

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

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(i) APPLICANTS: Wallner, Barbara P.  
Cooper, Kevin D.

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(ii) TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen Presenting Cell Driven Skin Conditions Using Inhibitors of the CD2/LFA-3 Interaction

(iii) NUMBER OF SEQUENCES: 8

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD  
(B) STREET: 60 State Street, Suite 510  
(C) CITY: Boston  
(D) STATE: Massachusetts  
20 (E) COUNTRY: USA  
(F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: PCT/US92/08755  
(B) FILING DATE: 06-OCT-1992

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/862,022  
(B) FILING DATE: 12-APR-1992

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/770,969  
(B) FILING DATE: 07-OCT-1991

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Myers, Louis (PLM)  
(B) REGISTRATION NUMBER: 35,965  
(C) REFERENCE/DOCKET NUMBER: BGP-111CP

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400  
(B) TELEFAX: (617) 227-5941

55 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 753 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..750

10

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 1..84

15

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 85..750

20

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..750  
 (D) OTHER INFORMATION: /note= "Human transmembrane LFA-3"

25

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION: 646  
 (D) OTHER INFORMATION: /note= "Transmembrane domain"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG  
 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val  
 -28            -25            -20            -15

48

35

GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA  
 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln  
 -10            -5            1

96

40

ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT  
 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn  
 5            10            15            20

144

45

GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA  
 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala  
 25            30            35

192

50

GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG  
 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg  
 40            45            50

240

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GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA  
 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr  
 55            60            65

288

TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT  
 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp  
 70            75            80

336

ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA	384
Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr	
85 90 95 100	
5 CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA	432
Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile	
105 110 115	
10 CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT	480
Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp	
120 125 130	
15 TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG	528
Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys	
135 140 145	
20 ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA	576
Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro	
150 155 160	
25 TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC	624
Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser	
165 170 175 180	
30 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA	672
Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala	
185 190 195	
35 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATT CTG AAA TGT	720
Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys	
200 205 210	
40 GAC AGA AAA CCA GAC AGA ACC AAC TCC AAT TGA	753
Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn	
215 220	

## (2) INFORMATION FOR SEQ ID NO:2:

40 (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 250 amino acids	
(B) TYPE: amino acid	
(D) TOPOLOGY: linear	
45 (ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
50 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val	
-28 -25 -20 -15	
55 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln	
-10 -5 1	
5 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn	
5 10 15 20	
Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala	
25 30 35	

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg  
 40 45 50

5 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr  
 55 60 65

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp  
 70 75 80

10 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr  
 85 90 95 100

Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile  
 15 105 110 115

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp  
 120 125 130

20 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys  
 135 140 145

Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro  
 150 155 160

25 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser  
 165 170 175 180

Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala  
 30 185 190 195

Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys  
 200 205 210

35 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn  
 215 220

## (2) INFORMATION FOR SEQ ID NO:3:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

50 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..720

55 (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 1..84

55 (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 85..720

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..720  
 5 (D) OTHER INFORMATION: /note= "Human PI-linked LFA-3"

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 568..720  
 10 (D) OTHER INFORMATION: /note= "Signal sequence for  
 PI-linkage"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15	ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val -28            -25            -20            -15	48
20	GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln -10            -5            1	96
25	ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn 5            10            15            20	144
30	GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala 25            30            35	192
35	GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg 40            45            50	240
40	GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr 55            60            65	288
45	TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp 70            75            80	336
50	ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr 85            90            95            100	384
55	CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile 105            110            115	432
60	CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp 120            125            130	480
65	TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys 135            140            145	528

ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro 150 155 160	576
5 TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser 165 170 175 180	624
10 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala 185 190 195	672
15 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATG TAT GCT TTT Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe 200 205 210	720
20 TAA	723

## 20 (2) INFORMATION FOR SEQ ID NO:4:

25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 240 amino acids (B) TYPE: amino acid (C) TOPOLOGY: linear	
30 (ii) MOLECULE TYPE: protein	
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val -28 -25 -20 -15	
40 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln -10 -5 1	
45 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn 5 10 15 20	
50 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala 25 30 35	
55 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg 40 45 50	
60 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr 55 60 65	
65 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp 50 70 75 80	
70 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr 85 90 95 100	
75 80 85 90 95 100	
80 85 90 95 100	
85 90 95 100	
90 95 100	
95 100	
100	
105 110 115	
110 115	
115	
120 125 130	
125 130	
130	

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys  
 135 140 145  
 5 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro  
 150 155 160  
 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser  
 165 170 175 180  
 10 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala  
 185 190 195  
 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe  
 15 200 205 210

## (2) INFORMATION FOR SEQ ID NO:5:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1056 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: cDNA  
  
 (ix) FEATURE:  
 30 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1053  
  
 (ix) FEATURE:  
 35 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 1..72  
  
 (ix) FEATURE:  
 40 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 73..1053  
  
 (ix) FEATURE:  
 45 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..1053  
 (D) OTHER INFORMATION: /note= "Human CD2"  
  
 (ix) FEATURE:  
 50 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 628..702  
 (D) OTHER INFORMATION: /note= "Transmembrane domain"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AGC TTT CCA TGT AAA TTT GTA GCC AGC TTC CTT CTG ATT TTC AAT  
 55 Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn  
 -24 -20 -15 -10

48

GTT TCT TCC AAA GGT GCA GTC TCC AAA GAG ATT ACG AAT GCC TTG GAA  
 Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu

96

-5

1

5

	ACC TGG GGT GCC TTG GGT CAG GAC ATC AAC TTG GAC ATT CCT AGT TTT			144
5	Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe			
	10	15	20	
	CAA ATG AGT GAT GAT ATT GAC GAT ATA AAA TGG GAA AAA ACT TCA GAC			192
	Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp			
	25	30	35	40
10	AAG AAA AAG ATT GCA CAA TTC AGA AAA GAG AAA GAG ACT TTC AAG GAA			240
	Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu			
	45	50	55	
15	AAA GAT ACA TAT AAG CTA TTT AAA AAT GGA ACT CTG AAA ATT AAG CAT			288
	Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His			
	60	65	70	
20	CTG AAG ACC GAT GAT CAG GAT ATC TAC AAG GTA TCA ATA TAT GAT ACA			336
	Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr			
	75	80	85	
25	AAA GGA AAA AAT GTG TTG GAA AAA ATA TTT GAT TTG AAG ATT CAA GAG			384
	Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu			
	90	95	100	
30	AGG GTC TCA AAA CCA AAG ATC TCC TGG ACT TGT ATC AAC ACA ACC CTG			432
	Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu			
	105	110	115	120
	ACC TGT GAG GTA ATG AAT GGA ACT GAC CCC GAA TTA AAC CTG TAT CAA			480
	Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln			
	125	130	135	
35	GAT GGG AAA CAT CTA AAA CTT TCT CAG AGG GTC ATC ACA CAC AAG TGG			528
	Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp			
	140	145	150	
40	ACC ACC AGC CTG AGT GCA AAA TTC AAG TGC ACA GCA GGG AAC AAA GTC			576
	Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val			
	155	160	165	
45	AGC AAG GAA TCC AGT GTC GAG CCT GTC AGC TGT CCA GAG AAA GGT CTG			624
	Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu			
	170	175	180	
50	GAC ATC TAT CTC ATC ATT GGC ATA TGT GGA GGA GGC AGC CTC TTG ATG			672
	Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu Leu Met			
	185	190	195	200
	GTC TTT GTG GCA CTG CTC GTT TTC TAT ATC ACC AAA AGG AAA AAA CAG			720
	Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln			
	205	210	215	
55	AGG AGT CGG AGA AAT GAT GAG GAG CTG GAG ACA AGA GCC CAC AGA GTA			768
	Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val			
	220	225	230	
	GCT ACT GAA GAA AGG GGC CGG AAG CCC CAC CAA ATT CCA GCT TCA ACC			816

Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr  
 235. 240 245

5 CCT CAG AAT CCA GCA ACT TCC CAA CAT CCT CCT CCA CCA CCT GGT CAT  
 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His 864  
 250 255 260

10 CGT TCC CAG GCA CCT AGT CAT CGT CCC CCG CCT CCT GGA CAC CGT GTT  
 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val 912  
 265 270 275 280

15 CAG CAC CAG CCT CAG AAG AGG CCT CCT GCT CCG TCG GGC ACA CAA GTT  
 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val 960  
 285 290 295

20 CAC CAG CAG AAA GGC CCG CCC CTC CCC AGA CCT CGA GTT CAG CCA AAA  
 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys 1008  
 300 305 310

25 CCT CCC CAT GGG GCA GCA GAA AAC TCA TTG TCC CCT TCC TCT AAT  
 Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn 1053  
 315 320 325

25 TAA 1056

(2) INFORMATION FOR SEQ ID NO:6:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

40 Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn  
 -24 -20 -15 -10

45 Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu  
 -5 1 5

50 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe  
 10 15 20

55 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp  
 25 30 35 40

60 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu  
 45 50 55

65 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His  
 60 65 70

70 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr  
 75 80 85

75 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu

	90	95	100
	Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu		
105	110	115	120
5	Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln		
	125	130	135
10	Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp		
	140	145	150
	Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val		
	155	160	165
15	Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu		
	170	175	180
	Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu Leu Met		
185	190	195	200
20	Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln		
	205	210	215
25	Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val		
	220	225	230
	Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr		
	235	240	245
30	Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His		
	250	255	260
	Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val		
265	270	275	280
35	Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val		
	285	290	295
40	His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys		
	300	305	310
	Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn		
	315	320	325

45 (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1050 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 55 (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..1041

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 1..84

5 (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 85..1041

10 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 85..1041  
 (D) OTHER INFORMATION: /note- "LFA3TIP"

15 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 360..361  
 (D) OTHER INFORMATION: /note- "LFA-3/IgG fusion point"

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG	GTT	GCT	GGG	AGC	GAC	GCG	GGG	CGG	GCC	CTG	GGG	GTC	CTC	AGC	GTG	48	
Met	Val	Ala	Gly	Ser	Asp	Ala	Gly	Arg	Ala	Leu	Gly	Val	Leu	Ser	Val		
-28	-25	-25	-20	-20	-15												
25	GTC	TGC	CTG	CTG	CAC	TGC	TTT	GGT	TTC	ATC	AGC	TGT	TTT	TCC	CAA	CAA	96
	Val	Cys	Leu	Leu	His	Cys	Phe	Gly	Phe	Ile	Ser	Cys	Phe	Ser	Gln	Gln	
	-10	-5	-5	-1													
30	ATA	TAT	GGT	GTT	GTG	TAT	GGG	AAT	GTA	ACT	TTC	CAT	GTA	CCA	AGC	AAT	144
	Ile	Tyr	Gly	Val	Val	Tyr	Gly	Asn	Val	Thr	Phe	His	Val	Pro	Ser	Asn	
	5	10	10	15	20												
35	GTG	CCT	TTA	AAA	GAG	GTC	CTA	TGG	AAA	AAA	CAA	AAG	GAT	AAA	GTT	GCA	192
	Val	Pro	Leu	Lys	Glu	Val	Leu	Trp	Lys	Lys	Gln	Lys	Asp	Lys	Val	Ala	
	25	30	30	35													
40	GAA	CTG	GAA	AAT	TCT	GAA	TTC	AGA	GCT	TTC	TCA	TCT	TTT	AAA	AAT	AGG	240
	Glu	Leu	Glu	Asn	Ser	Glu	Phe	Arg	Ala	Phe	Ser	Ser	Phe	Lys	Asn	Arg	
	40	45	45	50													
45	GTT	TAT	TTA	GAC	ACT	GTG	TCA	GGT	AGC	CTC	ACT	ATC	TAC	AAC	TTA	ACA	288
	Val	Tyr	Leu	Asp	Thr	Val	Ser	Gly	Ser	Leu	Thr	Ile	Tyr	Asn	Leu	Thr	
	55	60	60	65													
50	TCA	TCA	GAT	GAA	GAT	GAG	TAT	GAA	ATG	GAA	TCG	CCA	AAT	ATT	ACT	GAT	336
	Ser	Ser	Asp	Glu	Asp	Glu	Tyr	Glu	Met	Glu	Ser	Pro	Asn	Ile	Thr	Asp	
	70	75	75	80													
55	ACC	ATG	AAG	TTC	TTT	CTT	TAT	GTC	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	432
	Thr	Met	Lys	Phe	Phe	Leu	Tyr	Val	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	
	85	90	90	95													
60	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGG	CCG	TCA	GTC	TTC	CTC	TTC	CCC	480
	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	
	105	110	110	115													
65	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	
	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	

	120	125	130	
5	TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn 135 140 145			528
10	TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg 150 155 160			576
15	GAG GAG CAG TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val 165 170 175 180			624
20	CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser 185 190 195			672
25	AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys 200 205 210			720
30	GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp 215 220 225			768
35	GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe 230 235 240			816
40	TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu 245 250 255 260			864
45	AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe 265 270 275			912
50	TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly 280 285 290			960
	AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr 295 300 305			1008
	ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGAGTGCAG Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 310 315			1050

## (2) INFORMATION FOR SEQ ID NO:8:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 347 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val  
 -28 -25 -20 -15

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln  
 -10 -5 1

10 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn  
 5 10 15 20

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala  
 25 30 35

15 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg  
 40 45 50

20 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr  
 55 60 65

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp  
 70 75 80

25 Thr Met Lys Phe Phe Leu Tyr Val Asp Lys Thr His Thr Cys Pro Pro  
 85 90 95 100

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
 105 110 115

30 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
 120 125 130

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
 35 135 140 145

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
 150 155 160

40 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
 165 170 175 180

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
 185 190 195

45 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
 200 205 210

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp  
 50 215 220 225

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
 230 235 240

55 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
 245 250 255 260

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
 265 270 275

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
280 285 290

5 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
295 300 305

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
310 315